AMENDMENTS TO THE CLAIMS

1. (Previously presented) A method for single nucleotide polymorphism (SNP) typing which comprises the steps of:

simultaneously amplifying a plurality of nucleotide sequences, said plurality of nucleotide sequences comprising at least two sites of single nucleotide polymorphism using genomic DNA whose amount is 10-40 ng per 100 sites and a plurality of primer pairs; and

typing by an INVADER assay or by a TAQMAN PCR method for distinguishing the site(s) of single nucleotide polymorphism of nucleotide sequences amplified in the above amplification step using the amplified nucleotide sequences,

with the result that at least 98% of single nucleotide polymorphisms are detected.

2. (Previously presented) The method for SNP typing according to claim 1, wherein said step of amplifying employs a polymerase chain reaction using a hot start method.

3. (Original) The method for SNP typing according to claim 1, wherein said step of amplifying employs 50 pairs or more primers.

4. (Canceled)

5. (Currently Amended) A method for SNP typing which comprises the steps of:

simultaneously amplifying a plurality, up to ~~400~~100, of nucleotide sequences, said plurality of nucleotide sequences comprising at least one or more sites of single nucleotide polymorphism using genomic DNA whose amount is 10-40 ng and a plurality of primer pairs; and

typing for distinguishing the site(s) of single nucleotide polymorphism of nucleotide sequences amplified in the above amplification step using the amplified nucleotide sequences,

with the result that at least 98% of single nucleotide polymorphisms are detected.

6. (Previously presented) The method for SNP typing according to claim 5, wherein said step of amplifying employs a polymerase chain reaction using a hot start method.

7. (Previously presented) The method for SNP typing according to claim 5, wherein said step of amplifying employs 50 pairs or more primers.

8. (Previously presented) The method for SNP typing according to claim 6, wherein said step of amplifying employs 50 pairs or more primers.

9. (Previously Presented) A method for single nucleotide polymorphism (SNP) typing which comprises the steps of:

simultaneously amplifying a plurality of nucleotide sequences, said plurality of nucleotide sequences comprising at least two sites of single nucleotide polymorphism using genomic DNA whose amount is 0.1 ng to 0.4 ng per site and a plurality of primer pairs; and

typing by an INVADER assay or by a TAQMAN PCR method for distinguishing the site(s) of single nucleotide polymorphism of nucleotide sequences amplified in the above amplification step using the amplified nucleotide sequences,

with the result that at least 98% of single nucleotide polymorphisms are detected.

10 . (Currently Amended) A method for SNP typing which comprises the steps of:

simultaneously amplifying a plurality, up to ~~400~~100, of nucleotide sequences, said plurality of nucleotide sequences comprising at least one or more sites of single nucleotide polymorphism using genomic DNA whose amount is 0.1 to 0.4 ng per site and a plurality of primer pairs; and

typing for distinguishing the site(s) of single nucleotide polymorphism of nucleotide sequences amplified in the above amplification step using the amplified nucleotide sequences,

with the result that at least 98% of single nucleotide polymorphisms are detected.

11. (New) A method for SNP typing which comprises the steps of:

simultaneously amplifying up to 100 nucleotide sequences, said nucleotide sequences comprising at least one or more sites of single nucleotide polymorphism using 40 ng of genomic DNA and a plurality of primer pairs; and

typing for distinguishing the site(s) of single nucleotide polymorphism of nucleotide sequences amplified in the above amplification step using the amplified nucleotide sequences, with the result that at least 98% of single nucleotide polymorphisms are detected.